Amendments to the Specification:

Please replace the paragraph at page 1, line 22-page 2, line 16, with the following amended paragraph:

In average anti-Sm reactivity is found in 5-30% of patients with SLE, although the specific frequency will vary depending on the detection system and the ethnicity of the SLE population (Abuaf et al., 1990; Jaekel et al., 2001). The Sm-antigen is part of the spliceosomal complex that catalyzes the splicing of nuclear pre-mRNA (Seraphin, 1995; Lerner et al., 1980). The complex itself comprises at least nine different polypeptides with molecular weights ranging from 9-29.5 kDa [B (B1, 28 kDa), B' (B2, 29 kDa), N (B3, 29.5 kDa), Dl (16 kDa), D2 (16.5 kDa), D3 (18 kDa), E (12 kDa), F (11 kDa) and G (9 kDa)] (Hoch, 1994). All of those core proteins can serve as targets of the anti-Sm immune response, most frequently the B and D polypeptides, which are therefore considered the major antigens (Hoch, 1994; Brahms et al., 1997; Ou et al., 1997). However, SmBB' and Ul specific RNPs which are frequently the target of autoantibodies in patients with MCTD share crossreactive epitopes, consequently SmD is regarded as the most specific Sm- antigen (van Venrooij et al. , 1991; Hoch et al. , 1999). Within the SmD family the SmDl/D3 pattern is at least four times more common than SmDl/D2/D3 recognition with a pronounced immunoreactivity to SmDl (Hoch et al. , 1999). In epitope-mapping studies, several linear and conformational epitopes have been mapped on the SmB- and D-proteins (Rokeach et al. , 1992; Hirakata et al. , 1993). On SmDl and BB' the major reactivity was predominantly found in the C-terminal extensions (Rokeach et al. , 1992; Hirakata et al., 1993; Rokeach and Hoch, 1992). The epitope PPPGMRPP (SEQ ID NO: 2) that occurs three times within the C-terminal extensions of SmBB' was shown to crossreact with other prolin rich

structures of spliceosomal autoantigens such as the U1 specific antigens and of retroviral proteins such as p24 gag of HIV-1 (De Keyser et al., 1992). Follow-up studies and immunization experiments revealed that this motif is consistently the earliest detectable SmBB' epitope acting as starting point of epitope-spreading events within the BB' molecule and to the SmD-polypeptides (Arbuckle, 1999; Greidinger and Hoffman, 2001).

Please replace the paragraph at page 2, line 20-page 3, line 2, with the following amended paragraph:

One of the described B-cell epitopes on SmD3 (epitope 4; aa 104-126) displayed close homology to an antigenic region from the SmDl protein finally leading to crossreactivity (McClain et al., 2002). For diagnostic purposes a synthetic peptide corresponding to the C-terminal extension of SmDl was used to develop an ELISA system with diagnostic sensitivities and specificities ranging from 36-70% and from 91.7% and 97.2%, respectively (Riemekasten et al., 1998; Jaekel et al., 2001). Recently, it has been shown, that the polypeptides Dl, D3 and BB' contain symmetrical dimethylarginine (referred to herein as sdR or sDMA) constituting a major autoepitope within the C-terminus of SmDl (Brahms et al., 2000; Brahms et al., 2001). In one of these studies a synthetic peptide of SmDl (aa 95-119) containing sDMA demonstrated significant increased immunoreactivity compared to the non-modified peptide reflecting a conflict to previous data (Riemekasten et al., 1998; Brahms et al., 2000).

Please replace the paragraph at page 3, lines 29-30, with the following amended paragraph:

In a second aspect the S33 peptide comprises the amino acid sequence AARG sdR ~~sDMA~~ GRGMGRGNIF (SEQ ID NO: 1).

Please replace the paragraph at page 5, lines 2-4, with the following amended paragraph:

Figure 1. Epitope analysis of SmDl and SmD3. C-terminal extensions of SmD 1 (a) and SmD3 (b) were synthesized as peptide arrays (15mers ; aa offset) and probed with patient sera. Immunoreactive peptide no. 77 was further tested as mimotope variants (c)[[.]], wherein the following peptides are referenced:

In Fig. 1a:

#	Sequence	aa	SEQ ID NO:
1	DVEPKVKSKKREAVA	81-95	(SEQ ID NO: 6)
2	VEPKVKSKKREAVAG	83-97	(SEQ ID NO: 7)
4	PKVKSKKREAVAGRG	85-99	(SEQ ID NO: 8)
6	VKSKKREAVAGRGRG	87-101	(SEQ ID NO: 9)
8	SKKREAVAGRGRGRG	89-103	(SEQ ID NO: 10)
10	KREAVAGRGRGRGRG	91-105	(SEQ ID NO: 11)
12	EAVAGRGRGRGRGRG	93-107	(SEQ ID NO: 12)
14	VAGRGRGRGRGRGRG	95-109	(SEQ ID NO: 13)
16	GRGRGRGRGRGRGRG	97-111	(SEQ ID NO: 14)
18	GRGRGRGRGRGRGRG	99-113	(SEQ ID NO: 14)
20	GRGRGRGRGRGRGRG	101-115	(SEQ ID NO: 14)
22	GRGRGRGRGRGRGGP	103-117	(SEQ ID NO: 15)
24	GRGRGRGRGRGGPRR	105-119	(SEQ ID NO: 16)

In Fig. 1b:

#	Sequence	aa	SEQ ID NO:
75	QVAARGRGRGMGRGN	106-120	(SEQ ID NO: 17)
76	VAARGRGRGMGRGNI	107-121	(SEQ ID NO: 18)
77	AARGRGRGMGRGNIF	108-122	(SEQ ID NO: 19)
78	ARGRGRGMGRGNIFQ	109-123	(SEQ ID NO: 20)
79	RGRGRGMGRGNIFQK	110-124	(SEQ ID NO: 21)
80	GRGRGMGRGNIFQKR	111-125	(SEQ ID NO: 22)
81	RGRGMGRGNIFQKRR	112-126	(SEQ ID NO: 23)

In Fig. 1c:

Sequence	SEQ ID NO:
AARGRGRGMGRGNIF	SEQ ID NO: 4
AAsGRGRGMGRGNIF	SEQ ID NO: 24
AARGsGRGMGRGNIF	SEQ ID NO: 1
AARGRGsGMGRGNIF	SEQ ID NO: 25
AARGRGRGMGsGNIF	SEQ ID NO: 26

wherein s = symmetrical dimethylarginine (sdR).

Please replace the paragraph at page 8, line 19-page 9, line 3, with the following amended paragraph:

Binding experiments with peptides derived from SmD3 showed similar results. Only SmD3 peptides containing sDMA reacted with anti-Sm antibodies confirming the importance of the symmetric methylation of arginine residues (see figure lb). In contrast to SmDl, no control

serum (e.g. CEN) demonstrated antibody binding to SmD3 derived peptides reflecting a high specificity. One particular peptide (no. 77, ^{108}AAsdRGsdRGsdRGMGsdRGNIF^{122}) (SEQ ID NO: 3) was strongly recognized by three out of five anti-Sm sera. Using a mutational analysis in which arginine residues of ^{108}AARGRGRGMGRGNIF^{122} (SEQ ID NO: 4) were successively replaced by sDMA we were able to show that a mimotope peptide with a single dimethylated arginine residue at position 112 displayed immunoreactivity with all of the five anti-Sm sera (#36, #37, #31, #84, #Sm) but not with the controls (e.g. CEN; see figure lc.). Thus, by introducing only one sDMA and at a defined position (amino acid 112) of SmD3, it was possible to increase the sensitivity of this peptide (^{108}AARGsdRGRGMGRGNIF ^{122}; S33) (SEQ ID NO: 1) without a loss in specificity. This candidate peptide was subsequently synthesized as soluble antigen and used as substrate in ELISA.

Please replace the paragraph at page 9, lines 20-24, with the following amended paragraph:

A 15 amino acid soluble peptide displaying highest sensitivity and specificity in the SPOT-assay (^{108}AARGsdRGRGMGRGNIF^{122}) (SEQ ID NO: 1) was synthesized for technical reasons with an additional Cys at the C-terminus. This peptide was subsequently used to develop an ELISA system based on the general protocol of the Varelisa® tests (Pharmacia, Freiburg, Germany).

Please replace the paragraph at page 15, lines 14-20, with the following amended paragraph:

McClain and colleagues (2002) described four antigenic regions on SmD3 of which antigenic region 4 covers the area 104-126. In this invention peptides synthesized on pins were subjected to analysis but without using the modified form of arginine. In the present invention reactivity within this region was only found in case natural arginine was replaced by sDMA. These contradictory results might be explained by the use of different sera, methology and/or by the varying peptide length. Three out of five sera specifically recognized the peptide ^{108}AAsdRGsdRGsdRGMGsdRGNIF^{122} (SEQ ID NO: 3) of this example.

Please replace the paragraph at page 15, lines 21-29, with the following amended paragraph:

Interestingly, the dimethylation of only one arginine and at a defined position (aa 112) could further increase the sensitivity of this particular mimotope peptide without a loss in specificity. Based on this data a candidate peptide was used (^{108}AARGsdRGRGMGRGNIF^{122}) (SEQ ID NO: 1) to develop an ELISA system. The new anti-Sm assay (anti-S33) demonstrated a sensitivity of 14.9% and a specificity of 99. 7% for lupus resulting in a high positive (PPV; 93.7%) and negative predictive value (NPV; 80.2%) and thus a high diagnostic efficiency (80.7%). Therefore this test offers new opportunities for the diagnosis of systemic lupus erythrematosus, especially for the differentiation between SLE and MCTD as revealed by the correlation study.

Please replace the paragraph at page 16, lines 9-25, with the following amended paragraph:

EBV, EBNA and anti-SmD antibodies. Epitope-mapping studies on SmDl have identified an epitope-motif (aa 95-119) that cross-reacts with a homologue sequence 35-58 of the Epstein-Barr virus nuclear antigen 1 (EBNA-1) (Sabbatini et al., 1993; Sabbatini et al., 1993; Marchini et al., 1994). A more recent study has shown that this epitope also cross-reacts with a homologue region of SmD3 containing glycine arginine repeats (RGRGRGMGR) (SEQ ID NO: 5) (McClain et al., 2002). Moreover it became evident that GPRR (aa 114- 119 on SmDl) represents a common cross-reactive autoepitope motif, which is present not only on EBNA-1, but also on a variety of autoantigens including CENP-A, B, C, SmBB', SmDl and Ro-52, to term only a few (Mahler et al., 2001). Thus patients suffering from infectious mononucleosis or SLE related disorders might be tested false positive in ELISAs using the C-terminal extensions of SmDl or SmD3. Furthermore, several studies have suggested an influence of EBV on the development of Lupus-like conditions (James et al., 1997). Therefore, it is considered that the use of EBV positive sera as controls is an important finding towards a highly specific and reliable anti-SmD immunoassay. Among the 25 EBV disease controls presented, no false positive sample was found confirming the suggested high specificity of the anti-S33-abs assay. Unfortunately, Riemekasten and colleagues (1998) did not include this patient group in the evaluation of their test.